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For many years, circular RNAs (circRNAs) were considered as splicing byproducts because they were associated with low levels of expression. However, the development of high-throughput RNA sequencing and circRNAs-specific computational tools highlighted the abundance of these circRNAs in eukaryotic cells. These single-stranded RNAs are made of closed continuous loops lacking free ends and are generated during the splicing of pre-mRNA [1]. According to recent studies, circRNAs are mainly produced by exonic sequences of coding genes (exonic circRNAs) through an alternative splicing mechanism called "backsplicing". More precisely, the end of a "donor" exon is linked to the beginning of an upstream "acceptor" exon. More rarely, circRNAs can also be produced from intronic sequences (intronic circRNAs) from intronic lariat [1]. The specific conformation of circRNAs makes their detection, quantification and functional characterization difficult [2]. Several circRNA mechanisms of action were already identified. According to existing studies, circRNAs would mainly act as microRNAs sponges or by protein interactions [2]. Recent studies have also shown that some circRNAs are evolutionarily conserved [3].

To screen the exhaustive circRNAs genomic content, we analyzed Total-RNAseq data obtained from pig (sus scrofa) and bovine (bos taurus) testicular and liver tissues. In an attempt to obtain a comprehensive overview of circRNAs in those tissues we developped an approach with a detection step agnostic to genome annotation [4]. This approach enables us to quantify the relative proportion of exonic and intronic circRNAs from coding and non-coding genes, the variability between individuals, tissues and species. Differential recruitement of splice junctions for circular transcripts versus linear transcript is also addressed.

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